



#8

SEQUENCE LISTING

<110> Bayne, Marvin L.
 Conn, Gregory L.
 Thomas, Jr., Kenneth A.

<120> VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
 II

<130> 18199CB

<140> US 10/071,370

<141> 2002-02-08

<150> 09/326,879

<151> 1999-06-07

<150> 09/038,199

<151> 1998-03-10

<150> 08/299,185

<151> 1994-08-31

<150> 08/000,834

<151> 1993-01-05

<150> 07/586,638

<151> 1990-09-21

<160> 29

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<211> 577

<212> DNA

<213> rat

<220>

<221> CDS

<222> (5)...(577)

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Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu	
1 5 10 15	

ctg tac ctc cac cat gcc aag tgg tcc cag gct gca ccc acg aca gaa	97
Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu	
20 25 30	

ggg gag cag aaa gcc cat gaa gtg gtg aag ttc atg gac gtc tac cag	145
Gly Glu Gln Lys Ala His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
35 40 45	

cgc agc tat tgc cgt ccg att gag acc ctg gtg gac atc ttc cag gag 193
 Arg Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 tac ccc gat gag ata gag tat atc ttc aag ccg tcc tgt gtg ccc cta 241
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75
 atg cgg tgt gcg ggc tgc tgc aat gat gaa gcc ctg gag tgc gtg ccc 289
 Met Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro
 80 85 90 95
 acg tcg gag agc aac gtc act atg cag atc atg cgg atc aaa cct cac 337
 Thr Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 caa agc cag cac ata gga gag atg agc ttc ctg cag cat agc aga tgt 385
 Gln Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys
 115 120 125
 gaa tgc aga cca aag aaa gat aga aca aag cca gaa aat cac tgt gag 433
 Glu Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu
 130 135 140
 cct tgt tca gag cgg aga aag cat ttg ttt gtc caa gat ccg cag acg 481
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155
 tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag 529
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 160 165 170 175
 ctt gag tta aac gaa cgt act tgc aga tgt gac aag cca agg cgg tga 577
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg *
 180 185 190

<210> 2

<211> 190

<212> PRT

<213> rat

<400> 2

Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
 20 25 30
 Glu Gln Lys Ala His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg
 35 40 45
 Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
 50 55 60
 Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 65 70 75 80
 Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
 85 90 95

Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
 100 105 110
 Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
 115 120 125
 Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu Pro
 130 135 140
 Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys
 145 150 155 160
 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu
 165 170 175
 Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 3
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<400> 3
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 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca 96
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30
 gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc 144
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45
 cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa 192
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60
 gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt 240
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80
 ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc 288
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95
 aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat 336
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110
 tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg 384
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125

cct att ctg gag acg aca aag gca gaa agg agg aaa acc aag ggg aag 432
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
 130 135 140

agg aag caa agc aaa acc cca cag act gag gaa ccc cac ctg tga 477
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu *
 145 150 155

<210> 4
 <211> 158
 <212> PRT
 <213> rat

<400> 4
 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
 130 135 140
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu
 145 150 155

<210> 5
 <211> 417
 <212> DNA
 <213> rat

<220>
 <221> CDS
 <222> (1)...(417)

<400> 5
 atg ctg gcc atg aag ctg ttc act tgc ttc ttg cag gtc cta gct ggg 48
 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca 96
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30

gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc 144
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45

cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa 192
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60

gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt 240
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80

ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc 288
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95

aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat 336
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110

tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg 384
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125

cct att ctg gag acg aca aag gca gaa agg taa 417
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg *
 130 135

<210> 6

<211> 138

<212> PRT

<213> rat

<400> 6

Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg
 130 135

<210> 7

<211> 14

<212> PRT

<213> rat

<400> 7

Ala Pro Thr Thr Glu Gly Glu Gln Lys Ala His Glu Val Val

1

5

10

<210> 8

<211> 19

<212> PRT

<213> rat

<220>

<221> MOD_RES

<222> (7)...(7)

<223> Xaa = Unknown

<400> 8

Ala Leu Ser Ala Gly Asn Xaa Ser Thr Glu Met Glu Val Val Pro Phe

1

5

10

15

Asn Glu Val

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a

y=t,c

<400> 9

tttgtcgact yatggaygtn tayca

25

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a

y = t,c

r = a,g

<400> 10

cagagaattc gtcgacartc ngtrttyttr ca

32

<210> 11
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 11
gactcgagtc gacatcgatt tttttttttt ttttt 35

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 12
tttgtcgact cagagcggag aaagc 25

<210> 13
<211> 25
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<220>
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<400> 13
tttgtcgacg aaaatcactg tgagc 25

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 14
gactcgagtc gacatcg 17

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 15
tttgtcgaca acacaggacg gcttgaag 28

<210> 16
 <211> 28
 <212> DNA
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 <220>
 <223> oligonucleotide

 <400> 16
 tttgtcgaca tactcctgga agatgtcc 28

 <210> 17
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide

 <400> 17
 cttcatcatt gcagcagc 18

 <210> 18
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide

 <400> 18
 tttgtcgaca accatgaact ttctgc 26

 <210> 19
 <211> 26
 <212> DNA
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 <220>
 <223> oligonucleotide

 <400> 19
 tttgtcgacg gtgagaggtc tagttc 26

 <210> 20
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide

 <400> 20
 aaaatcagtt cgaggaaagg gaaagggta aaaacgaaag cgcaagaaat cccggtttaa 60
 atcctggagc gt 72

<210> 21
 <211> 25
 <212> PRT
 <213> rat

<400> 21
 Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys
 1 5 10 15
 Lys Ser Arg Phe Lys Ser Trp Ser Val
 20 25

<210> 22
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
 <223> n = t,c,g,a
 h = t,c,a
 y = t,c
 r = a,g

<400> 22
 tttgtcgaca tayathgcng aygarc

26

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
 <223> n = t,c,g,a
 r = a,g

<400> 23
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26

<210> 24
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 <212> DNA
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<220>
 <223> oligonucleotide

<400> 24

gactcgagtc gacatcgatt tttttttttt ttttt 35

<210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 25
 tttgtcgaca caccctaag aagtgtc 27

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 26
 tttgtcgaca acagcgactc agaagg 26

<210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 27
 tttgtcgaca ctgaatatat gagacac 27

<210> 28
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
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<400> 28
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<210> 29
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a

<400> 29

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26